

CACACNTCCCCTACACATAGATATACATACAAAATCACAGAAAGTAATAGATATGGCTAAGTTTGCTACCAT
M A K F A T I

CATCTCTTCTCTTTGCTGCTCTTGTCTCTCTTTGCTGCCCTTTGAAGCACCAACAATGGTGGATGCAAGGTT
I S L L F A A L V L F A A F E A P T M V D A R L
Δ

GTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGCAGAAA
C E R P S G T W S G V C G N N A C R N Q C R N

CCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCAGCTCACAAAATGTATTGTACTTCCCATG
L E R A E H G S C N Y V F P A H K C I C Y F P C

TTAATCTACCAAATCACTTTTGTGCTTGTGTGTATTTTACATGTTATGTGTTTATTACATGAAATAAG
*

TCTGTGTCATCCTTATGGGTGACCTTATGACATGTACCAGATATATCATATATGTATGTTGTTGTGTGT

GGCAATTATAAACTTTTATTTGTGGATGCAAAAAAAAAAAAAAAAAAAA

FIG. 1

| | |
|---------|--|
| Al yAFP | <u>MAKFATIIISLLFAALVLF</u> <u>AAFEAPT</u> <u>MDA</u> -RLCERPSGTWSGVCNNNACRNQC |
| Rs-AFP1 | <u>MAKFASIIALLFAALVLF</u> <u>AAFEAET</u> <u>VEA</u> <u>QKLCERPSGTWSGVCNNNACKNQC</u> |
| Rs-AFP2 | <u>MAKFASIIALLFAALVLF</u> <u>AAFEAET</u> <u>VEA</u> <u>QKLCQRP</u> SGTWSGVCNNNACKNQC ** * * |

| | | |
|---------|------------------|-------------|
| Al yAFP | RNLERAEHGSCNYVFP | PAHKCICYFPC |
| Rs-AFP1 | INLEKARHGSCNYVFP | PAHKCICYFPC |
| Rs-AFP2 | IRLEKARHGSCNYVFP | PAHKCICYFPC |

** * *

FIG. 2

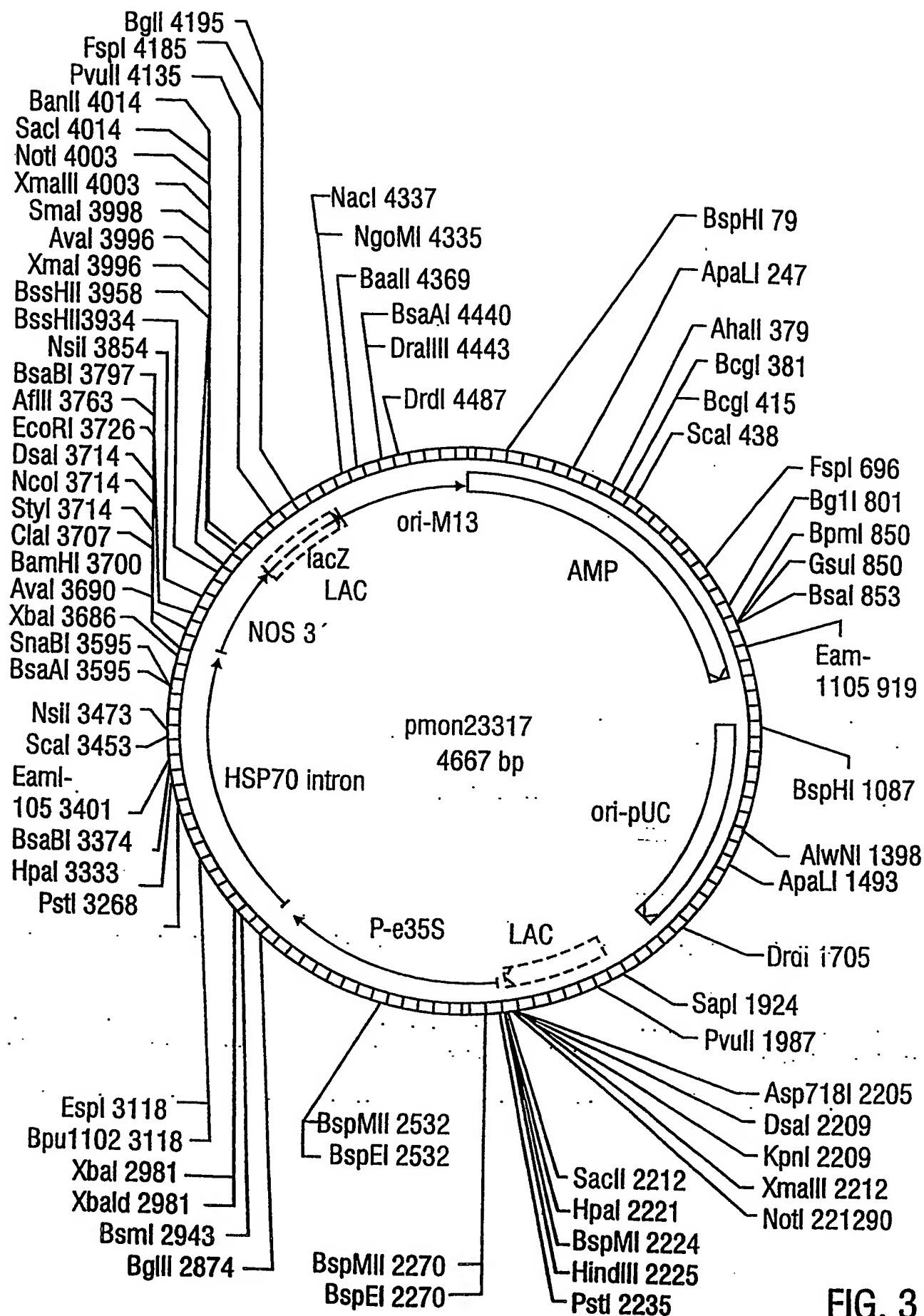


FIG. 3

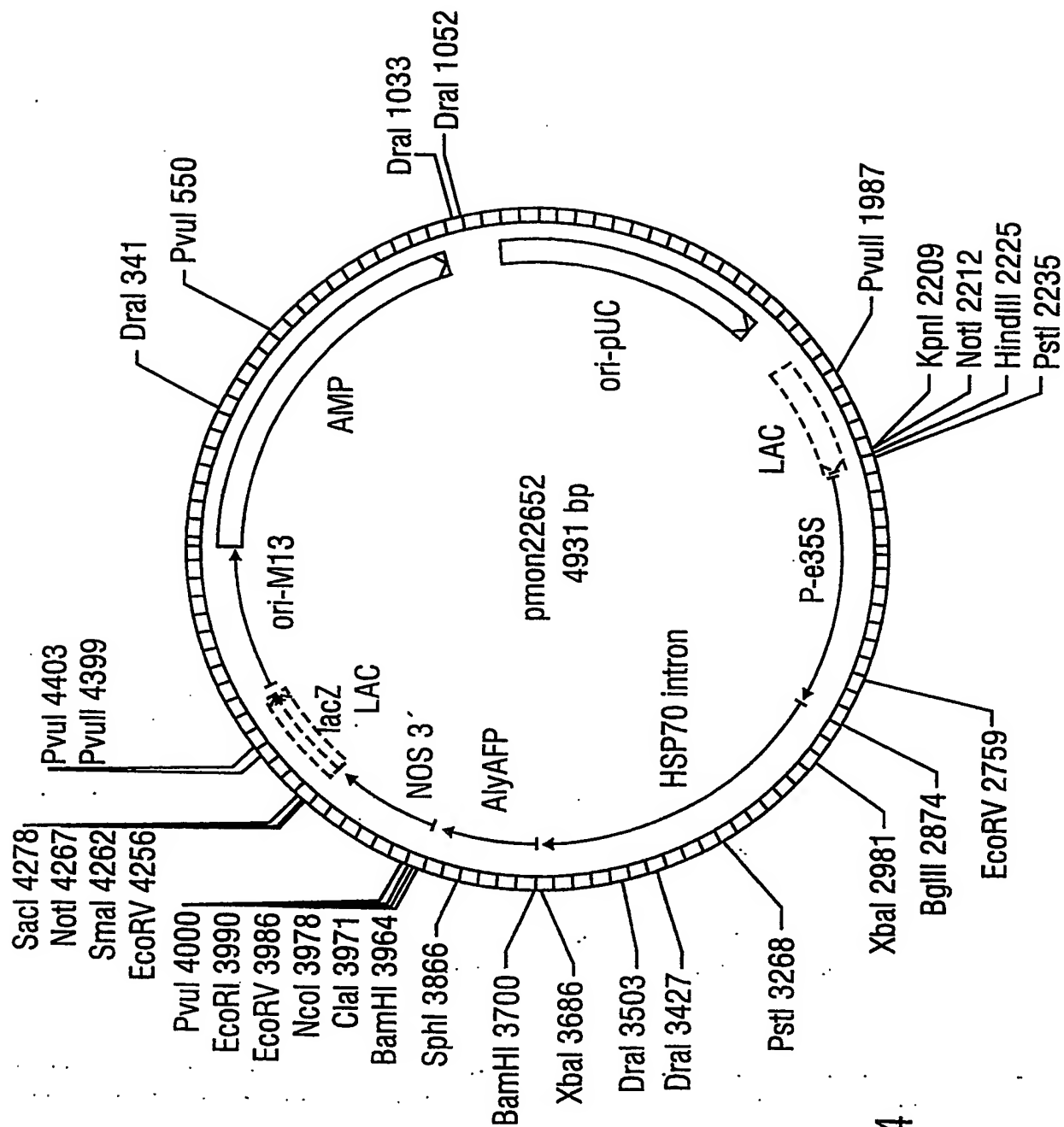


FIG. 4

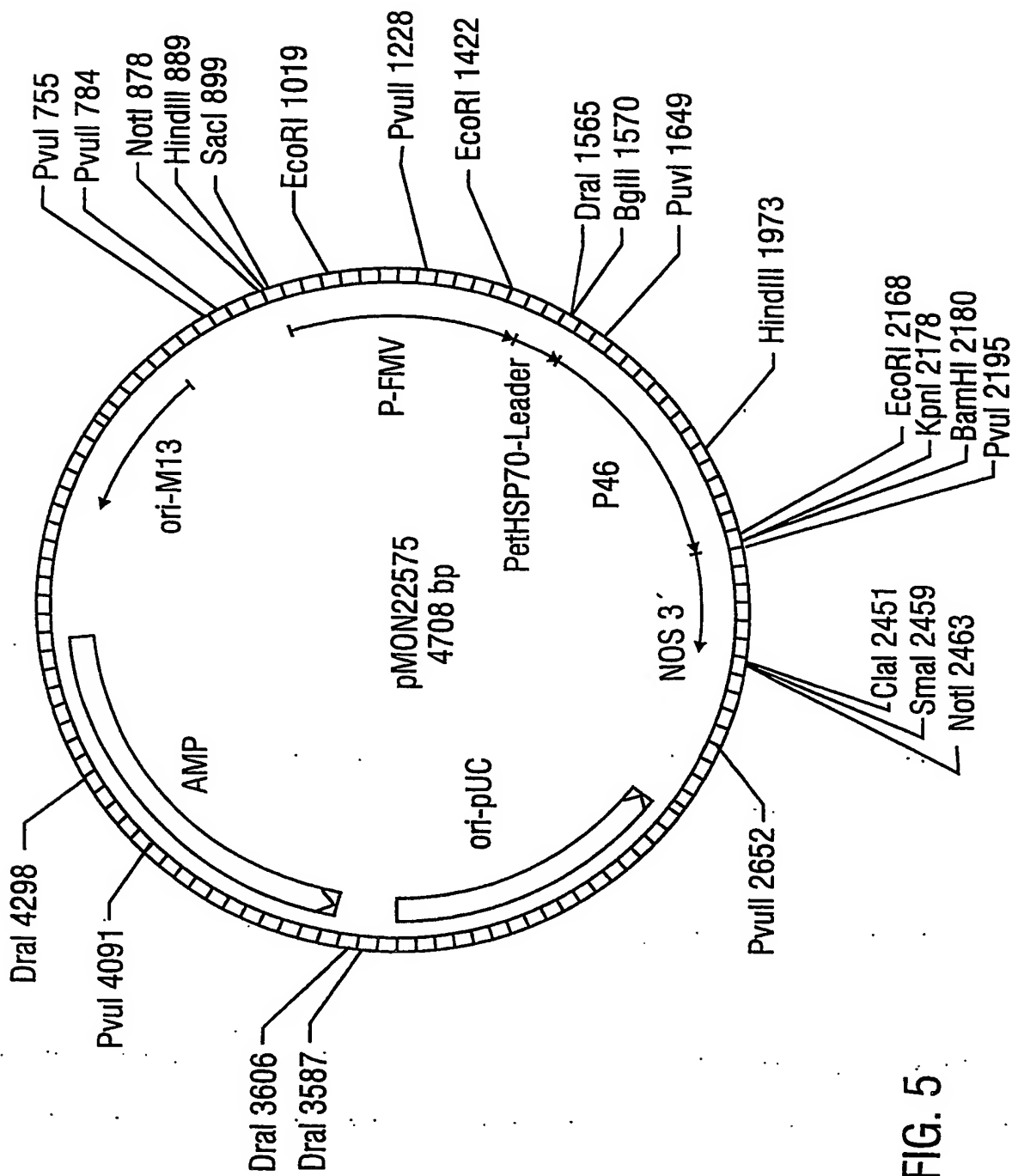


FIG. 5

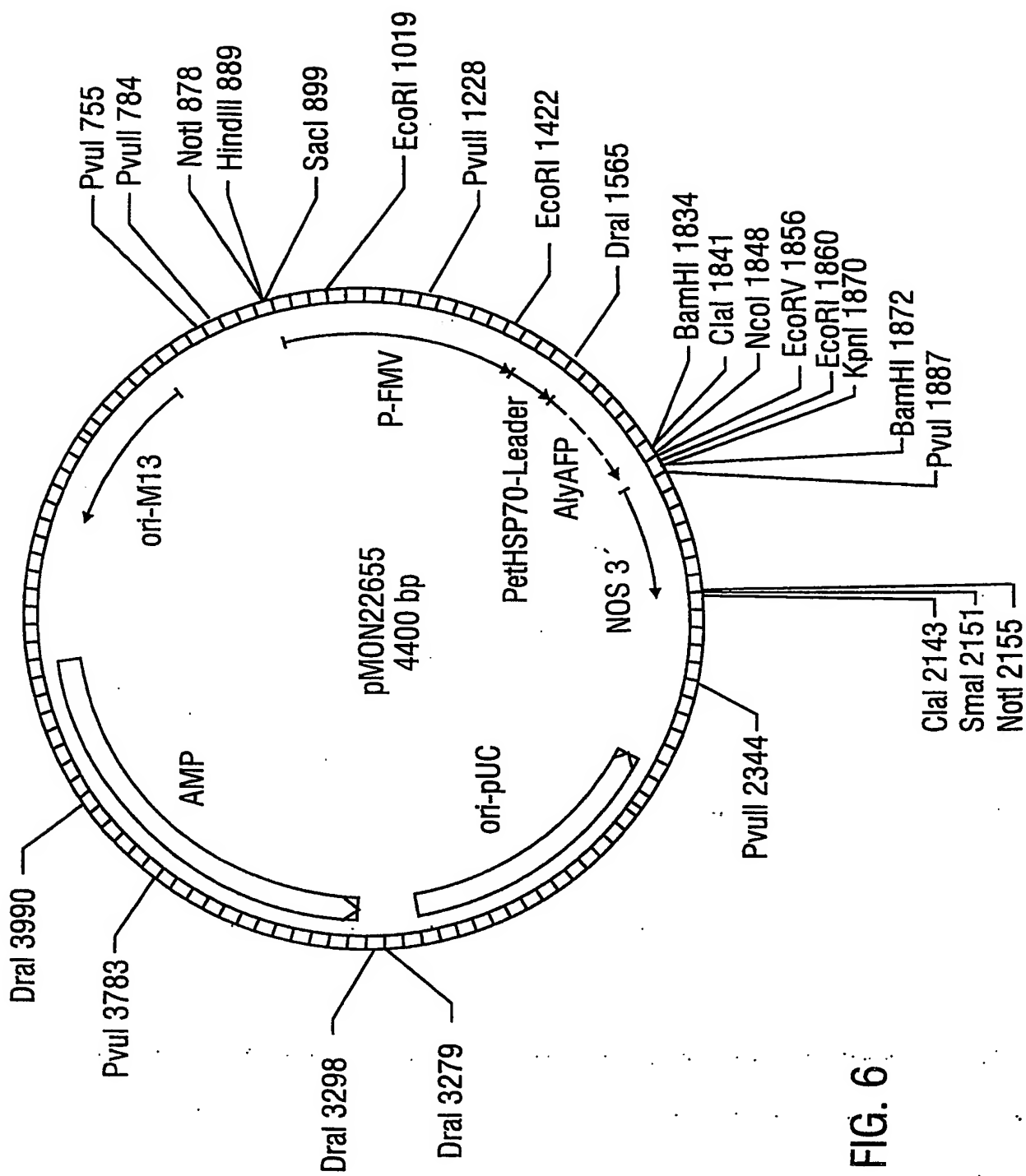


FIG. 6

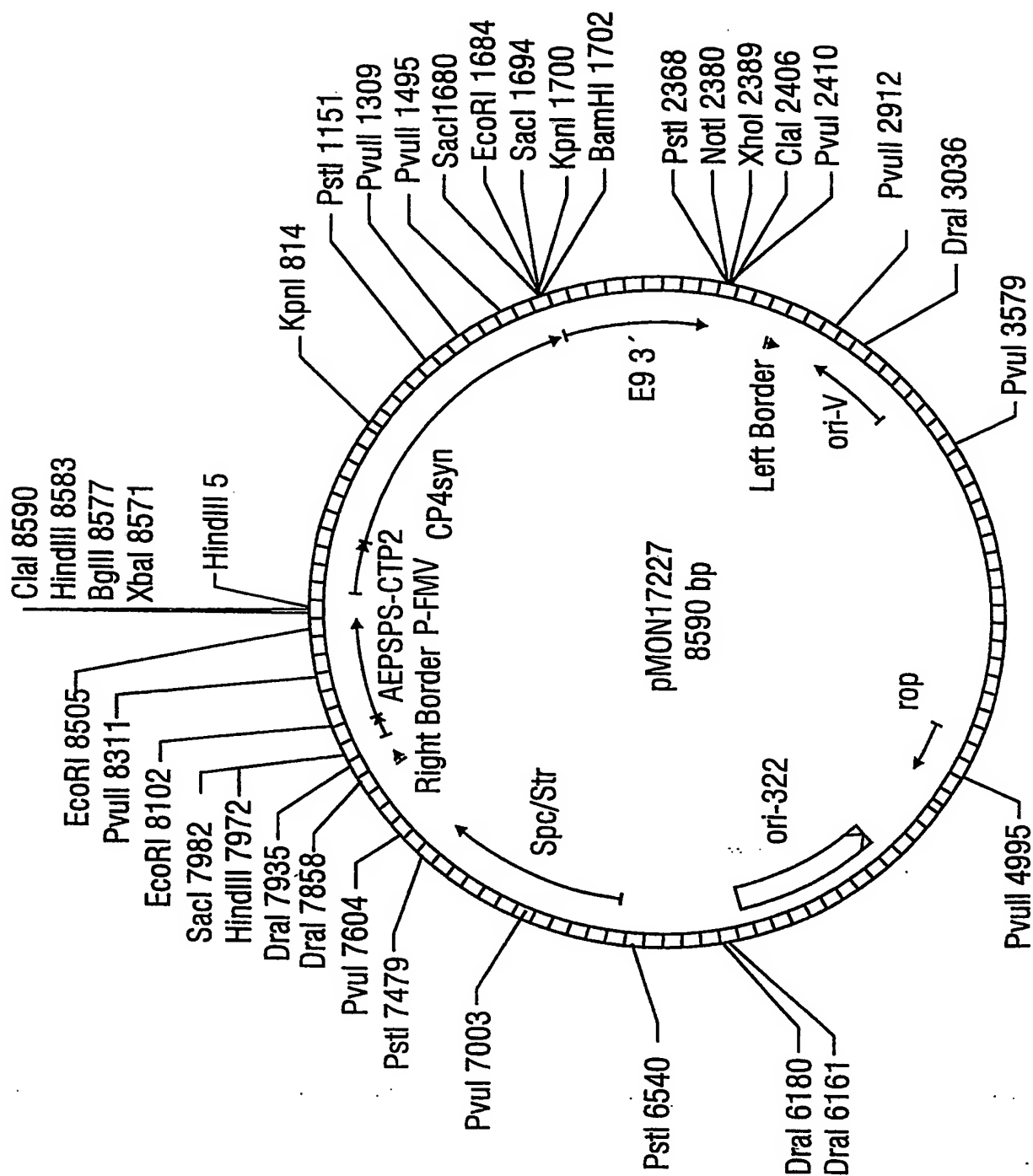


FIG. 7

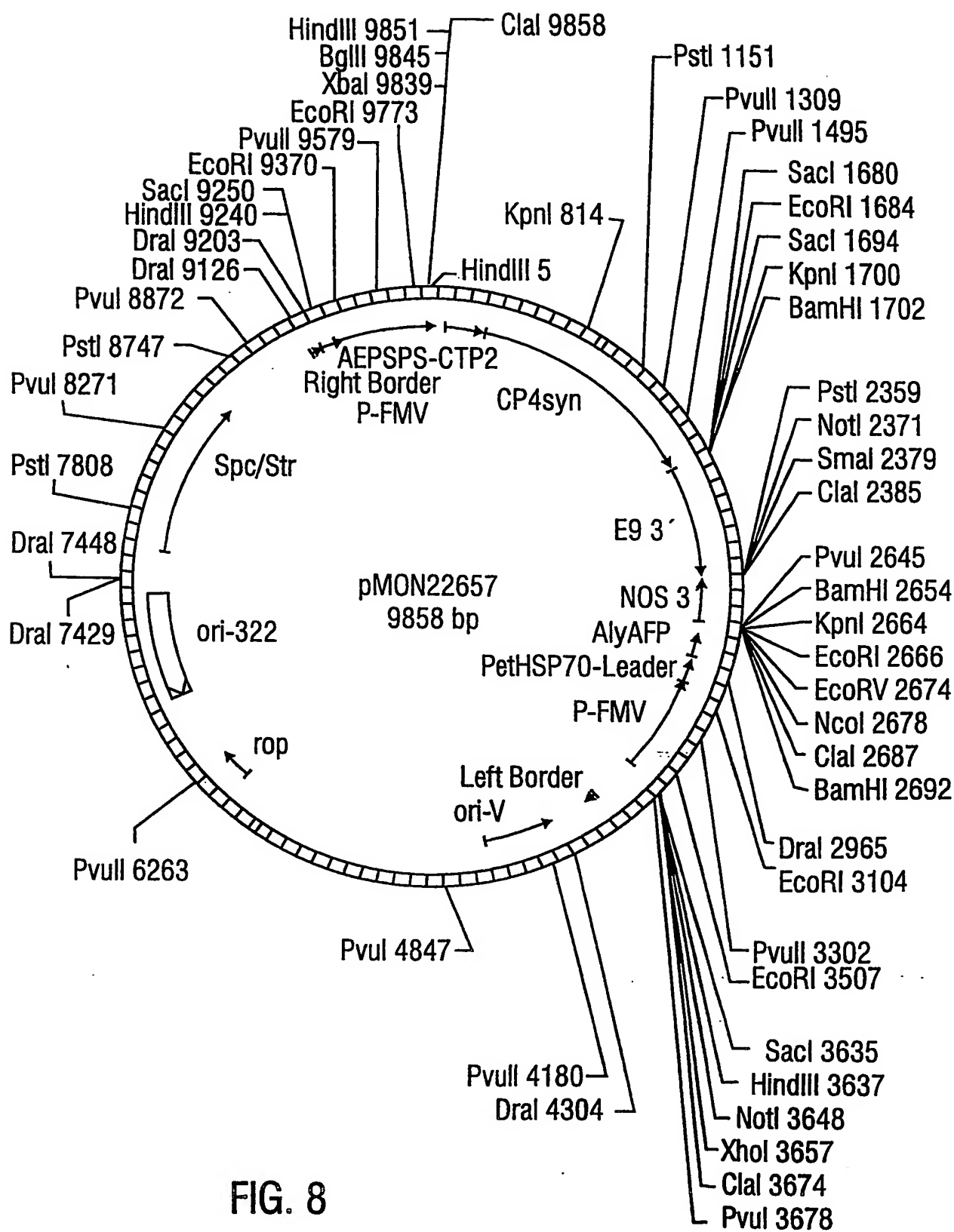


FIG. 8

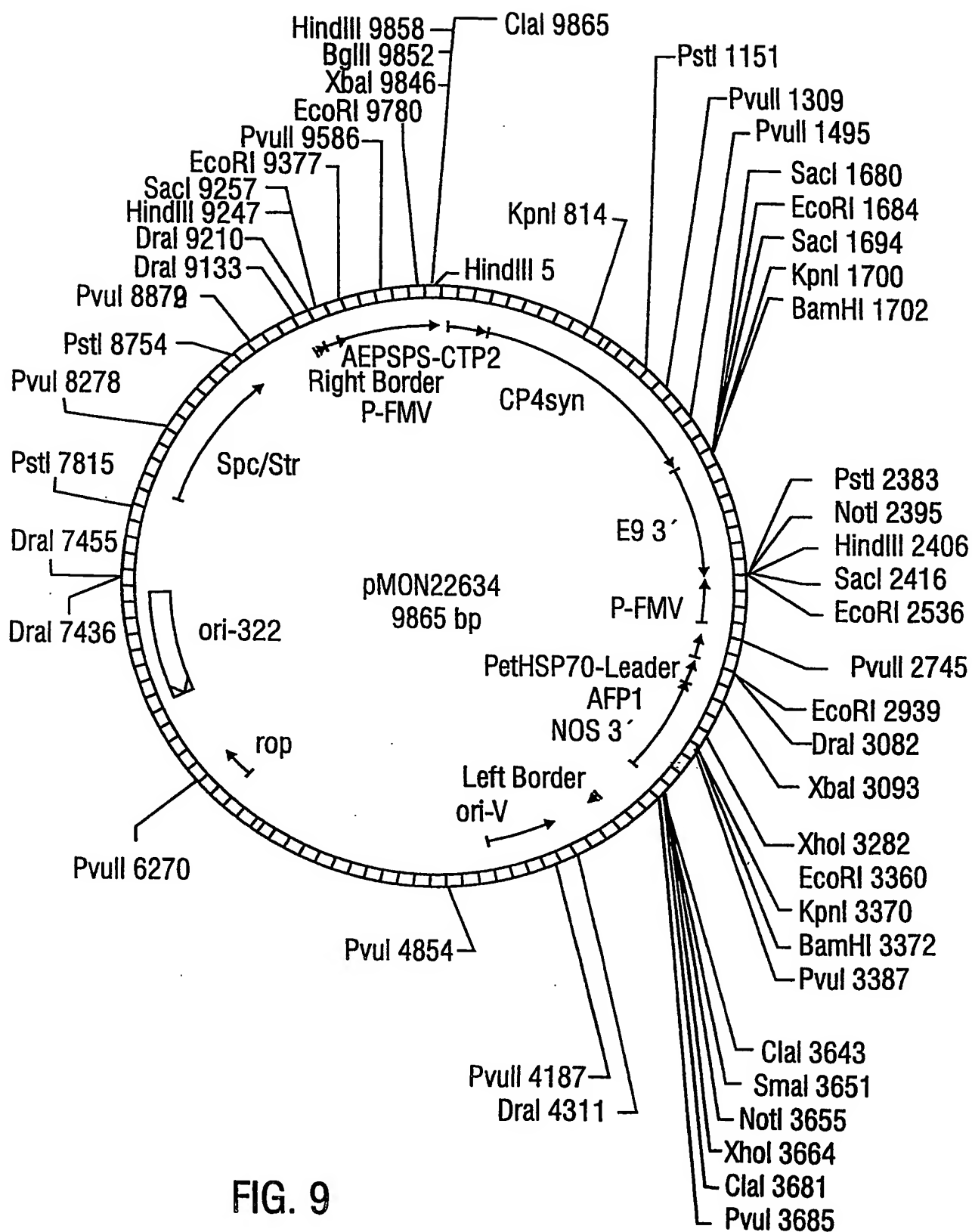


FIG. 9

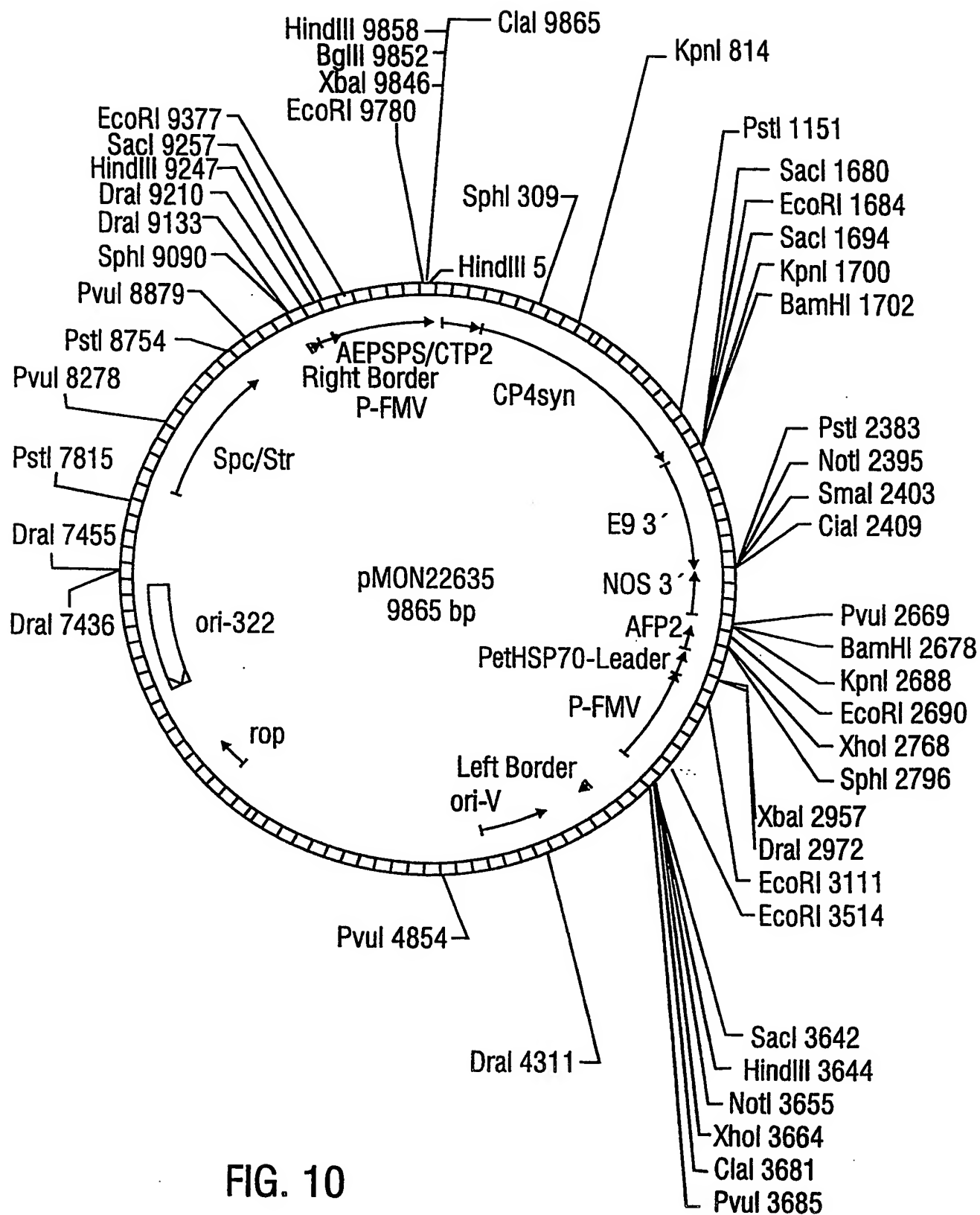


FIG. 10

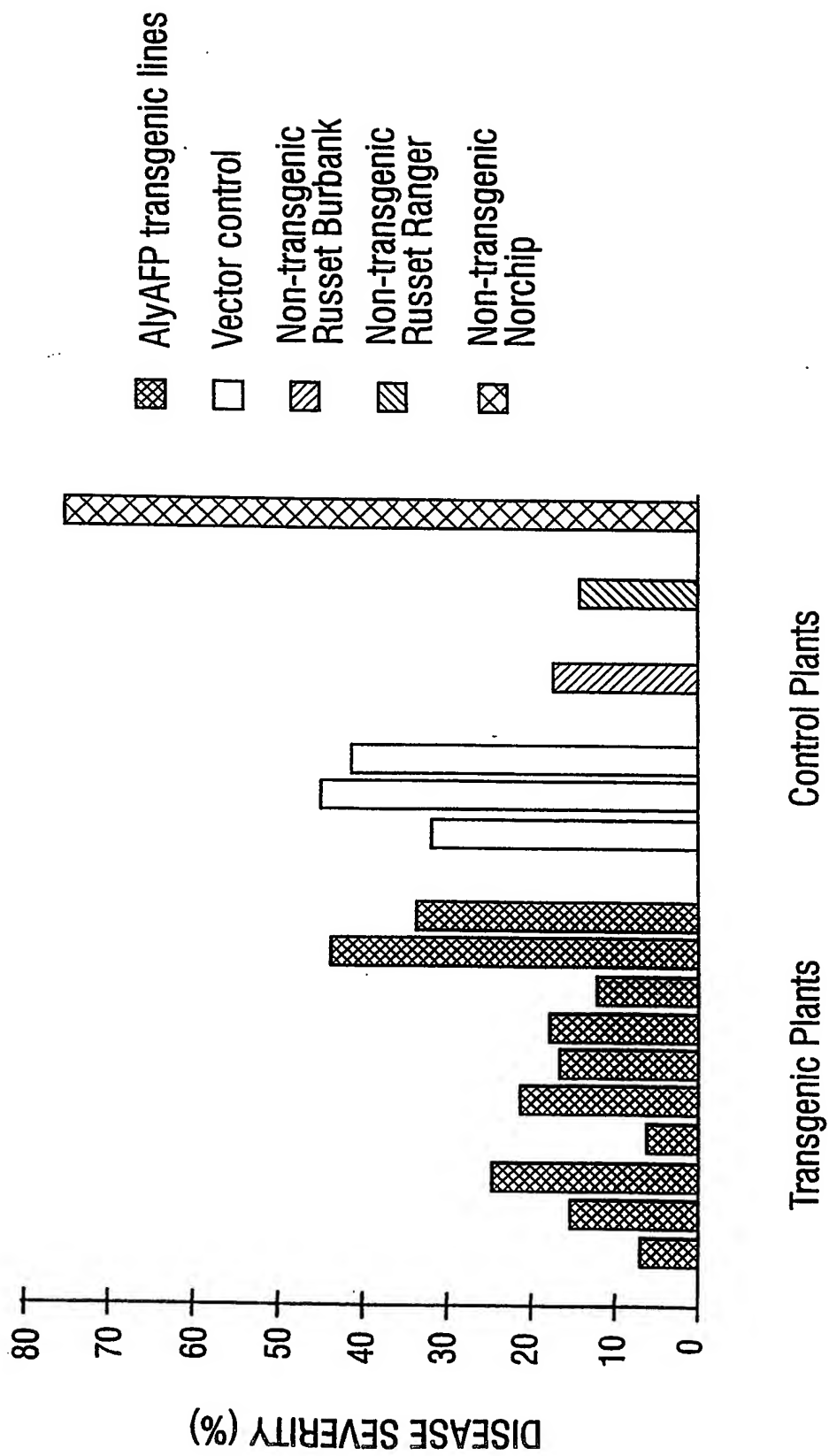


FIG.11

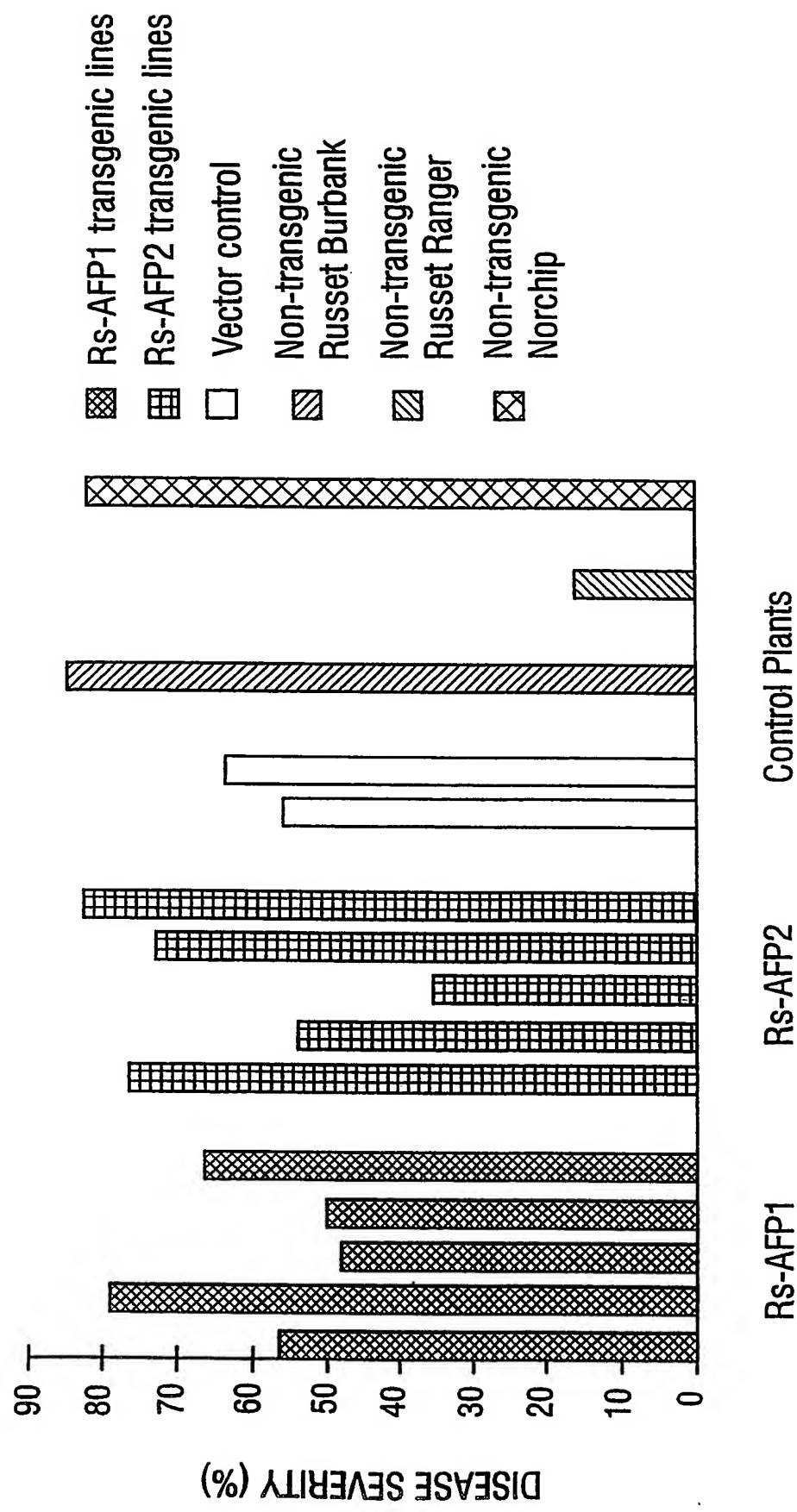


FIG.12